

7/7

Figure 5 (cont)

agaataatgtagttcggatccaacgggtgggtggattttcgaaatacacaaatgattcctcctccgat
gaacgggtacgatoagttatcttcttcaatcagatcatcatcagaggagccaagggtttcctttat
gatcatagaatcgctagaggagcttcagtttctgottctagtaactactattaatccttatttca
acgaggcaacaaatcatacgggtactaagtatagttccattttattaatactcattataggtatat
atgtatataactgttgatcttatttgatttaactgggtgggttttagggagccaatggagggaatttg
ggagctacatggaaggaaaccctagaaatggatcaggagggtgtgaaggagtacgaggttttttcc
ggggaaatatggtgaaagagtttcagtggtgggttaaaaogtctgtoactcgttaggtgattgcagt
cotaataccattgattttgtccttgaagcttt~~aaa~~atgttttatctttctatattgatttaaaaca
aatcgtctcttttaagaaaaaacatttttaagtagatgaaagtaagaaacagaaagaaaaaaaga
gagagccttttttgggtgtatgcacatctgagagctgagtcgaagaaagattcagctttttggatta
cccttttgggtgtttattatgagattotaacctaaacactcagacatatatgtttctgttctctt
ccttaattgttgtcatgaaacttctc

FIG. 5 (cont)

ttcccttctctctctcttatotaaaaagagttccggagagaagaagatcatcatcaatggogacttct
ctcttctttoatgtcaacagatcaaaaactccgctcggaaccccaaacgatcttcttgagaaacaccc
gtcttgtcgtcaacagctccggcgagatccggacagagacactgaagagtcgtggtcggaaccc
aggatcgaagacaggtcagcaaaaacagaagaaaccaacggttgagaggaatgggtgtagcaaaag
ctcgagcgtcagagaaatcgaagaagaaaagaagcaactcgcgcgcgcacagtccggagacacgt
catcagtagcatcgatctcttaacaacgotaacccgtttaaccgtacccggtagacccgggtgttgt
gctacaaggcttcccaagctcactcggggagcaacaggatctattgtggtggagtcgggtcgggt
cagggttatgatcgacccgggttatttctccatgggggttttgttgagacctcctccactactcatg
agctctcttcaatctcaaatcctcaaatgtttaaacgttcttcccaantaatcgctgtgacacttg
cttcaagggttgtttgttttttaatcgttttcatcaacatgattgatataatataagtttttgc
acttgaaaaagttttgatttttatttcatgtaaaaaactgcagaagaacagtttggatggtgac

41

5/7

FIGURE 5

-2690

cggaatcccaagaatctttctatgcctgcctaaaccoagcaatataaatcaaaccttcacacgct
tcgggtctctcttttacacgtgccggaaaaaaaccctagtagtagccgcccaatgaccatctaaa
gtgggtcccgatgatgacacgtgtcagttggaccactatccgtaacttaacatgaaagcacatgt
gggggtccctcttttcgtccctttgccctaccagttcccttgctctagcccacaatacaatctacggt
gtatctatatcaaagtttatctagctatcttccgaaatagaaagcatataacttccatttatttt
tgaacaaattaaacttggttagaaataaaatctttcgatattgatttatttcgatttagtgtaac
tctattatcatctcgtgtgtcattctaggcttatagcaacagtgtaggtatgttgcaatgttgg
gttgggtcatgccgtttggatttatttccagtgattaattcagattttatttttcttcttaatta
tctacgtataacaaaatctcgttaaccgcagagtgaaattgcatgtcactcatgaatgttttga
gtataagaagttagtaatttgttttataaatatatgaacttatgaagatacatattgaagttgt
tttgtttgggggtaaaaaagggttatttgagtggttatatgataactttactcagaaaacgtaact
agcaaaggtaattcgaagtacctttggaatcgagtaaaatactgataactagaaaaataagata
cataatggagaaataattaaatatatttgatttcttttttgtttaacaacgtacgttttatta
ttagctagtatacatattacaacggttacgtagatcatataatagccatttaagatgtacaacat
ctcatctgggttacttcatattatataaaaaaaaaaacgaaatctcaacacatagtaattgtataatt
acttcagtggggtctctcttaagacttgatttgagaatatccatataaaaacaaactttgtatta
agataattaaaaattttctaatagttaggtattggggtgaagccaagattaacatggaggcagctt
taaaatgtttccttatatgatgcagccatcatttctactctactccgtagctccaaaccttct
cgtaattcacgtctctcatgctattctttttgctttcgctcctctctcatgtgaagcaataact
atctctcgatttttttttcaaataccgaaagctaactttttcaaataaatgtcaaatatatta
atcttcgttttgtatttagtattttatttgctcagctaagtatagtgagtttttaagcttactcg
tcgtatttatcatatattcatatacatatcacattagtcaaagtaataaaaaattgtttttga

4/7

AP3	1	MARGKIKIKRIENQINRQ
DEFA	1	MARGKIKIKRIENQINRQ
AG_	1	SGRGKIKIKRIENTINRQ
MCM1	1	KERRKIKIKFIENKTRRH
SRF	1	RGRVKIKKEFIENKLRRY
GLO	1	MGRGKIKIKRIENSINRQ
RLM1-yeast	1	MGRRKIKIKIRISIDDRNRA
SMP1-yeast	1	MGRRKIKIKIEPIKIDRNRT
MEF2D	1	MGRKKIKIKIRITIERNRQ
AGL5	1	MGRGKIKIKRIENANSRQ
FBP11	1	MGRGKIKIKRIENNTINRQ
BOAP1	1	MGRGKIKIKRIENKINRQ
AGL11	1	MGRGKIKIKRIENSTINRQ
SPL	1	MGVAKKEERQRIEIEE-KKQ

Figure 4

Figure 1. The 12 test items of the TAP. The items are arranged in a vertical column, showing various patterns of dots and lines representing different test stimuli.

3/7

Met Ala Thr Ser Leu Phe Phe Met Ser Thr Asp Gln Asn Ser Val Gly Asn Pro Asn Asp
1 5 10 15 20
Leu Leu Lrg Asn Thr Arg Leu Val Val Asn Ser Ser Gly Glu Ile Arg Thr Glu Thr Leu
25 30 35 40
Lys Ser Arg Gly Arg Lys Pro Gly Ser Lys Thr Gly Gln Gln Lys Gln Lys Lys Pro Thr
45 50 55 60
Leu Arg Gly Met Gly Val Ala Lys Leu Glu Arg Gln Arg Ile Glu Glu Glu Lys Lys Gln
65 70 75 80
Leu Ala Ala Ala Thr Val Gly Asp Thr Ser Ser Val Ala Ser Ile Ser Asn Asn Ala Thr
85 90 95 100
Arg Leu Pro Val Pro Val Asp Pro Gly Val Val Leu Gln Gly Phe Pro Ser Ser Leu Gly
105 110 115 120
Ser Asn Arg Ile Tyr Cys Gly Gly Val Gly Ser Gly Gln Val Met Ile Asp Pro Val Ile
125 130 135 140
Ser Pro Trp Gly Phe Val Glu Thr Ser Ser Thr Thr His Glu Leu Ser Ser Ile Ser Asn
145 150 155 160
Pro Gln Met Phe Asn Ala Ser Ser Asn Asn Arg Cys Asp Thr Cys Phe Lys Lys Lys Arg
165 170 175 180
Leu Asp Gly Asp Gln Asn Asn Val Val Arg Ser Asn Gly Gly Gly Phe Ser Lys Tyr Thr
185 190 195 200
Met Ile Pro Pro Pro Met Asn Gly Tyr Asp Gln Tyr Leu Leu Gln Ser Asp His His Gln
205 210 215 220
Arg Ser Gln Gly Phe Leu Tyr Asp His Arg Ile Ala Arg Ala Ala Ser Val Ser Ala Ser
225 230 235 240
Ser Thr Thr Ile Asn Pro Tyr Phe Asn Glu Ala Thr Asn His Thr Gly Pro Met Glu Glu
245 250 255 260
Phe Gly Ser Tyr Met Glu Gly Asn Pro Arg Asn Gly Ser Gly Gly Val Lys Glu Tyr Glu
265 270 275 280
Phe Phe Pro Gly Lys Tyr Gly Glu Arg Val Ser Val Val Ala Thr Thr Ser Ser Leu Val
285 290 295 300
Gly Asp Cys Ser Pro Asn Thr Ile Asp Leu Ser Leu Lys Leu
305 310

FIG. 3

CAGACTTAAAGCTTTCGTCTTTACCTCTTECCTTCTCTCTCTATCTAAAAAGAGTTCCGAGA	64
AGAAGATCATCATCAATGGCGACTTCTCTCTTCTTCATGTCAACAGATCAAACTCCGTCGGAA	128
ACCCAAACGATCTTCTGAGAAACACCCGTCTTGTCTGTCATAGCTCCGGCGAGATCCGGACAGA	192
GACACTGAAGAGTCGTGGTCGGAAACAGGATCGAAGACAGGTCAGCAAAAAACAGAAGAAACCA	256
ACGTTGAGAGGAATGGGTGTAGCAAAGCTCGAGCGTCAGAGAATCGAAGAAGAAAGAAGCAAC	320
TCGCCGCCGCCACAGTCGGAGACACGTCATCAGTAGCATCGATCTCTAACAACGCTACCCGTTT	384
ACCCGTACCCGTAGACCCGGGTGTTGTCTACAAGGCTTCCCAAGCTCACTCGGGAGCAACAGG	448
ATCTATTGTGTGTCGAGTCGGGTCTGGGTCTAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTT	512
TTGTTGAGACCTCCTCCACTACTCATGAGCTCTCTTCAATCTCAAATCCTCAAATGTTTAACGC	576
TTCTTCCAATAATCGCTGTGACACTTGCTTCAAGAAGAAACGTTTGGATGGTGATCAGAATAAT	640
GTAGTTCGATCCAACGGTGGTGGATTTTCGAAATACCAATGATTCCTCCTCCGATGAACGGCT	704
ACGATCAGTATCTTCTTCAATCAGATCATCATCAGAGGAGCCAAGGTTTCTTTATGATCATAG	768
AATCGCTAGAGCAGCTTCAGTTTCTGCTCTAGTACTACTATTAATCCTTATTTCAACGAGGCA	832
ACAAATCATACGGGACCAATGGAGGAATTTGGGAGCTACATGGAAGGAAACCTAGAAATGGAT	896
CAGGAGGTGTGAAGGAGTACGAGTTTTTCCGGGGAAATATGGTGAAAGAGTTTCAGTGGTGCC	960
TACAACGTCGTCACCTCGTAGGTGATTGCAGTCTTAATACCATGATTGTCTTGAAGCTTTAA	1024
ATGTTTTATCTTTCTATATTGATTTAAACAAATCGTCTCTTTAAAGAAAAAACATTTTAAGTA	1088
GATGAAAGTAAGAAACAGAAGAAAAAAGAGAGAGCCTTTTTTGGTGTATGCATCTGAGAGCT	1152
GAGTCGAAAGAAAGATTGAGCTTTTGGATTACCTTTTGGTTGTTTATTATGAGATTCTAACCT	1216
AAACACTCAGACATATATGTTCTGTTCTCTTCTTAAATTGTTGTCATGAACTTCTCAAAAAA	1280
AAAAAAAAAAAAAAAAAAAAA	1302

FIG. 2

09/701023

5' of the SPL gene

gtagcatcga tctctaacaa cgctacccgt ttaccctgtac cggtagaccc ggggtgttgc 59

3' of Ds element

gcta<<<cagggat gaaaacggtc ggtaacggtc ggtaaaatac-----

-----Ds element-----

tacgggattt ttcccatcct actttcatcc cgg>>>gcacaa ggcttcccaa

5' of Ds element

gctcatcggg agcaacagga tctattgtgg tggagtcggg tcgggtcagg ttatgatcga
cccggttatt tctccatggg gttttgttga gacctcctcc actactcatg agctctcttc a

FIG. 1A.

cagggat gaaaacggtc ggtaacggtc ggtaaaatac tacgggattt ttcccatcct
actttcatcc cgg

FIG. 1B.

09/701023

WO 00/56907

PCT/SG99/00023

7/7

Figure 5 (cont)

agaataatgtagttcgatccaacgggtgggtggattttcgaaatacacaaatgattcctcctccgat
gaacgggctaagatacgtatcttcttcaatcagatcatcatcagaggagccaagggttctctttat
gatcatagaatcgctagagcagcttcagtttctgottctagtaactactattaatccttatttca
acgaggcaacaaatcatacgggtactaagttatagtcattttattaatactcataatatagggtatat
atgtatataactggtgatcttatttgatttaactgggtgggtttagggaccaatggaggaatttg
ggagctacatggaaggaaaccctagaaatggatcaggagggtgtgaaggagtacgagttttttcc
ggggaaatatggtgaaagagtttccagtggtggctaaaaagtcgtcactcgtaggtgattgcagt
cctaataccattgattttgtccttgaagctttaaagtttttatcttcttatattgatttaaaaca
aatcgtctcttttaagaaaaaacatttttaagtagatgaaagttaagaaacagaagaaaaaaaaga
gagagccttttttgggtgtatgcacatctgagagctgagtcgaaagaaagattcagcttttggatta
cccttttgggtgtttattatgagattctaaccctaaacactcagacatatatgtttctgttctctt
ccttaattgttgtcatgaaacttctc

09701023-001301

WO 00/56907

PCT/SG99/00023

6/7

Figure 5 (cont)

agaaaaaaaaatacatataactgcgagctctgcgactgtaactggacttgcttatttttagttga
tatgagctgagtaaaatcacgttggtccagaccttgctcgctacaatcggcgaatgggtctaacg
tcccgacacctgtcctcgatccgcgggtaactatattctttgcaatgtgatgcacgcgctgttac
tattggacagtgtttctcacctcacgactgagcctatgcgagtagcgacaatctccgatttgct
gtctccatggtagggattatcacaaatctctgattttttttatcaggaacaagtaaaataaatagc
tttgagttttttgtttttttctacattctctcgcccaaaagatgtaagaaaataaaggatttgaa
acctgtgtctgtgtgttactccttttaaatctcttaaaaactataaatcattatatctttgatctgt
ttcacaaactaatcatattcggttgcaaagtgagaattcggtccacctttactctttacaccgata
ctagtattatagatgtacagcatagttatccatatctagttatttagtcaaaactctatatatt
aagaggtaggttaattaattaaggagtaattgaagattatagaaagaataaaaaataaccattta
atggacagaaccaaagataactaactatcatactataatgttgaaattcttccacgatccaatg
catggataacaacatcaatcaaatcatacattcatgctatataacatagttttcagttacaaac
tctcttttttatttatttcagttgttcttttcatgaccatattaacatcaaataatgcatttt
tttcaacgtctcttgacttacaccactaatattgacaaatlgaacatctatcgactatacac
acataagttaaaaatgcatgcaagtgttaagggaatttataacatctaagggttaataagactaa
gaaagtataaaaaataagaatacgtattatgaatttatgatatactttactaatctttttgaaaaa
tactttaatttaactactatagggggtaaaaaagtaaaaaagaaataaagatacgtttatccgc
atatagtacctggaataacagaaaaataaaaacacaggttaagtactttgcctgagctagtatat
gaacactaaagagatacacacacacaaaaagagagcagaaacaaaacacacacacttaaaagctt
tcgtctttacctc

#1

ttcccttctctctctcttatotaaaaagagttccgagaagaagatcatcatcaatggogacttct
ctcttcttctatgtcaacagatcaaaactccgtcggaaccccaaacgatcttctgagaaacaccc
gtcttgctgctcaacagctccggcgagatccggacagagacactgaagagtcgtgggtcggaaccc
aggatcgaagacaggtcagcaaaaacagaaagaaacccacgttgagaggaatgggtgtagcaaaag
ctcgagcgtcagagaatcgaagaagaaaagaagcaactcgccgcgcacagtcggagacacgt
catcagtagcatcgatctcttaacaacgctacccgtttaaccgtaccggtagacccgggtgttgt
gctacaaggcttcccaagctcactcgggagcaacaggatctattgtgggtggagtcgggtcgggt
caggttatgatcgaccgggttatttctccatgggggttttgggtgagacctcctccactactcatg
agctctcttcaatctcaaatcctcaaatgtttaogettcttccaataatcgctgtgacacttg
cttcaagggttggtgtgttttttaacgttttcatcaacatgattgatataatagtttttgc
acttgaaaaagtttgatttttatttatgtaaaaaactgcagaagaaacgttttggatggtgatc

FIGURE 5

-2690

cggatcccaagaatctttctatgcctgcctaaacccagcaatataaatcaaaccttcacacgct
tcggttcttcttttacacgtgccggaacccctagtagtagccgcccaatgaccatctaaa
gtggtccccgtgatgacacgtgtcagttggaccactatccgtaacttaacatgaaagcacatgt
ggggtccctctttcgctctttgccctaccagttccttgctctagcccacatacaatctacgcg
gtatctatatcaaagtttatctagctattttccgaaatagaagcatataacttccatttatttt
tgaacaaattaaacttggtagaaataaaatctttcgatattgatttatttccgatttagtgtaat
tctattatcatctcgctgtcatttctaggcttatagcaacagtgtaggtatggttgcaatggttg
gttggtcatgccgtttggatttatttccagtgattaattcagattttatttttcttcttaatta
tctacgtataacaaaatctcgctaaccgcagagtgaatttgcattgctactcatgaatgttttga
gtataagaagtgaagtaatttgttttataaatatatgaacttatgaagatacatattgaagttgt
tttgtttgggggtaaaaaagggttatttgcagtggtatatgataactttactcagaaaacgtaact
agcaaaggtaattcgaagtacctttggaatcgagtaataactgataactagaaaaataagata
cataatggagaaaataattaaatatatttgtatttcttttttgtttaacaacgtacgttttatta
ttagctagtatacatttacaacgggtacgtagatcatataatagccatttaagatgtacaacat
ctcatctggttacttcatttatataaaaaaaaaaacgaaatctcaacacatagtaattgtataatt
acttcagtggggcttctcttaagacttgtatttgagaatatccatataaaaacaaactttgtatta
agataattaaaaattttctaattagtaggtattgggctgaagccaagattaacatggaggcagctt
taaaatgtttcttatatgatgcagccatcatttctactctactccgtagctccaaaccccttct
cgtaattcaegtcctctcatgctattctttttgctttcgtctcctctcatgtgaagcaataact
atctctcgatttttttttcaaataccgaaagctaactttttcaaataaatgtcaaatatatta
attttcgttttgtatttagtattttatttgcagctaagtatagttagtattttaagcttactcg
tcgtatttatcatatattcatatacatatcacattagtcaaagtaataaaaaatttgtttttga

09/701023-061001

WO 00/56907

PCT/SG99/00023

4/7

AP3	1	W	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
DEFA	1	W	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
AG	1	S	G	R	G	K	I	E	I	K	R	I	E	N	T	N	R	Q	
MCM1	1	K	E	R	R	K	I	E	I	K	F	I	E	N	K	T	R	R	H
SRF	1	R	G	R	V	K	I	E	I	K	E	I	E	N	K	L	R	R	Y
GLO	1	W	G	R	G	K	I	E	I	K	R	I	E	N	S	N	R	Q	
RLM1-yeast	1	W	G	R	R	K	I	E	I	Q	R	I	S	D	R	N	R	A	
SMP1-yeast	1	W	G	R	R	K	I	E	I	E	P	I	K	D	R	N	R	T	
MEF2D	1	W	G	R	K	K	I	E	I	Q	R	I	T	E	R	N	R	Q	
AGL5	1	W	G	R	G	K	I	E	I	K	R	I	E	N	A	N	S	R	Q
FBP11	1	W	G	R	G	K	I	E	I	K	R	I	E	N	N	T	N	R	Q
BOAP1	1	W	G	R	G	K	I	E	I	K	R	I	E	N	K	I	N	R	Q
AGL11	1	W	G	R	G	K	I	E	I	K	R	I	E	N	S	T	N	R	Q
SPL	1	W	G	V	A	K	E	R	Q	R	I	E	E	E	-	K	R	Q	

Figure 4

09/701023

3/7

Met Ala Thr Ser Leu Phe Phe Met Ser Thr Asp Gln Asn Ser Val Gly Asn Pro Asn Asp
1 5 10 15 20
Leu Leu Lrg Asn Thr Arg Leu Val Val Asn Ser Ser Gly Glu Ile Arg Thr Glu Thr Leu
25 30 35 40
Lys Ser Arg Gly Arg Lys Pro Gly Ser Lys Thr Gly Gln Gln Lys Gln Lys Lys Pro Thr
45 50 55 60
Leu Arg Gly Met Gly Val Ala Lys Leu Glu Arg Gln Arg Ile Glu Glu Glu Lys Lys Gln
65 70 75 80
Leu Ala Ala Ala Thr Val Gly Asp Thr Ser Ser Val Ala Ser Ile Ser Asn Asn Ala Thr
85 90 95 100
Arg Leu Pro Val Pro Val Asp Pro Gly Val Val Leu Gln Gly Phe Pro Ser Ser Leu Gly
105 110 115 120
Ser Asn Arg Ile Tyr Cys Gly Gly Val Gly Ser Gly Gln Val Met Ile Asp Pro Val Ile
125 130 135 140
Ser Pro Trp Gly Phe Val Glu Thr Ser Ser Thr Thr His Glu Leu Ser Ser Ile Ser Asn
145 150 155 160
Pro Gln Met Phe Asn Ala Ser Ser Asn Asn Arg Cys Asp Thr Cys Phe Lys Lys Lys Arg
165 170 175 180
Leu Asp Gly Asp Gln Asn Asn Val Val Arg Ser Asn Gly Gly Gly Phe Ser Lys Tyr Thr
185 190 195 200
Met Ile Pro Pro Pro Met Asn Gly Tyr Asp Gln Tyr Leu Leu Gln Ser Asp His His Gln
205 210 215 220
Arg Ser Gln Gly Phe Leu Tyr Asp His Arg Ile Ala Arg Ala Ala Ser Val Ser Ala Ser
225 230 235 240
Ser Thr Thr Ile Asn Pro Tyr Phe Asn Glu Ala Thr Asn His Thr Gly Pro Met Glu Glu
245 250 255 260
Phe Gly Ser Tyr Met Glu Gly Asn Pro Arg Asn Gly Ser Gly Gly Val Lys Glu Tyr Glu
265 270 275 280
Phe Phe Pro Gly Lys Tyr Gly Glu Arg Val Ser Val Val Ala Thr Thr Ser Ser Leu Val
285 290 295 300
Gly Asp Cys Ser Pro Asn Thr Ile Asp Leu Ser Leu Lys Leu
305 310

FIG. 3

CAGACTTAAAGCTTTCGTCTTTACCTCTTECCTTCTCTCTCTATCTAAAAAGAGTTCCGAGA	64
AGAAGATCATCATCAATGGCGACTTCTCTCTTCTTCATGTCAACAGATCAAAACTCCGTCCGAA	120
ACCCAAACGATCTTCTGAGAAACACCCGTCTTGTCGTCAATAGCTCCGGCCAGATCCGGACAGA	192
GACACTGAAGAGTCGTGGTCGGAAACCCAGGATCGAAGACAGGTGAGCAAAAACAGAAGAAACCA	256
ACGTTGAGAGGAATGGGTGTAGCAAAGCTCGAGCGTCAGAGAATCGAAGAAAGAAAGCAAC	320
TCGCCGCCGCCACAGTCGGAGACACGTCATCAGTAGCATCGATCTCTAACACGCTACCCGTTT	384
ACCCGTACCCGTAGACCCGGGTGTTGTGCTACAAGGCTTCCCAAGCTCACTCGGGAGCAACAGG	448
ATCTATTGTGGTGGAGTCGGGTCCGGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTT	512
TTGTTGAGACCTCCTCCACTACTCATGAGCTCTCTCAATCTCAAATCCTCAAATGTTTAAAGC	576
TTCTTCCAATAATCGCTGTGACACTTGCTTCAAGAAGAAACGTTTGGATGGTGATCAGAATAAT	640
GTAGTTCGATCCAACGGTGGTGGATTTTCGAAATACACAATGATTCCCTCCGATGAACGGCT	704
ACGATCAGTATCTTCTTCAATCAGATCATCATCAGAGGAGCCAAGGTTTCCTTTATGATCATAG	768
AATCGCTAGAGCAGCTTCAGTTTCTGCTTCTAGTACTACTATTAATCCTTATTTCAACGAGGCA	832
ACAAATCATACGGGACCAATGGAGGAATTTGGGAGCTACATGGAAGGAAACCTAGAAATGGAT	896
CAGGAGGTGTGAAGGAGTACGAGTTTTTCCGGGGAATATGGTGAAAGAGTTTCAGTGGTGGC	960
TACAACGTCGTCCTCGTAGGTGATTGCAGTCTCTTAATACCATTGATTTGTCTTGAAGCTTTAA	1024
ATGTTTTATCTTTCTATATTGATTTAAACAAATCGTCTCTTTAAAGAAAAAACATTTTAAAGTA	1088
GATGAAAGTAAGAAACAGAAGAAAAAAGAGAGAGCCTTTTTGGGTGATGCATCTGAGAGCT	1152
GAGTCGAAAGAAAGATTACGCTTTTGGATTACCTTTTTGGTTGTTTATTATGAGATTCTAACCT	1216
AAACACTCAGACATATATGTTCTGTTCTCTTCTTAATTGTTGTCATGAAACTTCTCAAAAAA	1280
AAAAAAAAAAAAAAAAAAAAA	1302

FIG. 2

09/701023-061604

5' of the SPL gene

gtagcatcga tctctaacaa cgctaccegt ttaccctgac cggtagaccc ggggtgttgc 59

3' of Ds element

gcta<<<cagggat gaaaacggtc ggtaacggtc ggtaaaatac-----

-----Ds element-----

tacgggattt ttcccatcct actttcatcc cgg>>>gctacaa ggcttcccaa

5' of Ds element

gctcatcggg agcaacagga tctattgtg tggagtcggg tcgggtcagg ttatgatcga
cccggttatt tctccatggg gttttgttga gacctcctcc actactcatg agctctcttc a

FIG. 1A.

cagggat gaaaacggtc ggtaacggtc ggtaaaatac tacgggattt ttcccatcct
actttcatcc cgg

FIG. 1B.

09/701023